patients and healthy control groups. IL17A serum levels and clinical and laboratory parameters were measured using the enzyme-linked immune sorbent assay (ELISA) technique.

Results: RA patients showed higher IL 17A serum levels than the control group (121.9 ± 24.3 ng/dl vs 20.4 ± 2.6 ng/dl, P < 0.001). RA patients showed a higher frequency of rs2275913 G allele than healthy subjects (P = 0.01). Patients carrying GG genotype showed higher values of all disease severity parameters including Rheumatoid Factor (52.79 ± 16.65 IU/ml, P < 0.001) and Anti-Cyclic Citrullinated Peptide Antibody (30.6 ± 14.86 U/ml, P < 0.001). The high-risk GG genotype carriers had higher IL17A serum levels than the GA and AA genotypes carriers (129.74 ± 23.03 ng/dl vs 107.49 ± 19.85 ng/dl, P <0.001).

Conclusion: The major allele of IL17A rs2275913 polymorphism was associated with higher IL17A serum levels, and greater RA activity. It is thus very likely that the rs2275913 polymorphism of IL17A gene is associated with an increased risk of RA, as well as with higher severity in Egyptian RA patients.

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**AB0003**

**INTERLEUKIN 17A RS2275913 GENE POLYMorphism IS RELATED TO SEVERITY AND DISEASE ACTIVITY OF Rheumatoid arthritis AND INCREASED SERum IL17A LEVELS IN EGYPTIAN PATIENTS.**

**Keywords:** Cytokines and chemokines, Rheumatoid arthritis, Genetics/Epigenetics

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**Backround:** Interleukin 17A (IL17A), one of the IL-17 family, performs a critical role in the inflamed synovial tissue of Rheumatoid Arthritis (RA) patients. Several studies have been performed to investigate the role of IL 17A rs2275913 polymorphism in RA pathogenesis, however, data about its role in RA severity and activity is inconsistent.

**Objectives:** We aimed to investigate the influence of IL17A rs2275913 polymorphism on IL17A serum levels in Egyptian RA patients and disease severity and activity.

**Methods:** The study included 100 healthy subjects and 100 RA patients. Genotype polymorphism rs2275913 was measured by Taqman genotyping assay in both
novel Bioinformatic tools may assist in the better understanding of this polygenic disease, while its association with RA and other ADs is a helpful step towards comprehending the shared biological pathways leading to autoimmunity. The data resulting from our study can be utilized towards the development of an application designed to assist clinical diagnosis by using the patients' genomic data, like the integrated bioinformatics tools Demetra for endometriosis [6] and Epione for SLE [7].

REFERENCES:

Results: Consistent with the observed diversity trend, compared with periodontal health, the richness of patients with periodontitis is relatively high (P<0.05, Figure 1a), which indicates that the diversity of salivary microbiome in patients with periodontitis is significantly higher. The Beta diversity based on Bray Curtis distance at the species level demonstrated a significant difference in microbial communities between periodontitis patients and periodontal health (analysis of variance, r2=0.094, p=0.001, Figure 1b). At different phylogenetic levels, the 10 selected taxonomic biomarkers showed strong discrimination ability, with log10 LDA score >4.0 (Figure 1c-d). Specifically, at the phylum level, the Firmicutes/phylum frequency of periodontitis patients is lower, while the Spirochaetota frequency is higher. Patients with periodontitis have more genus Treponema at the genus level (Figure 1c-d). PICRUSt analysis found that in the KEGG pathway, the function of microbial genes related to amino acid metabolism in the salivary microbiota of periodontitis patients was higher (Figure 1h). Treponema was positively correlated with periodontal probing depth (PPD), Total, plaque index (PI) and periodontitis extent Ca. Sipirochaetota was positively correlated with PPD Total, PI (p<0.05, Figure 1i).

Conclusion: Specific salivary microbiota played an important role in the pathogenesis of periodontitis, which may help to diagnose or determine individual susceptibility to periodontitis by detecting salivary microbiota.

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Figure 1. Functional network of the 9 common genes between RA and MG as generated by GeneMANIA.

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AB0005

CHANGES OF SALIVARY MICROBIAL COMMUNITY IN PATIENTS WITH PERIODONTITIS

Keywords: Prognostic factors, Adaptive immunity, Biomarkers

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Background: Periodontitis (PD) is a chronic, progressive polymicrobial disease[1]. In the context of the microbiome in the pathogenesis of rheumatic disease, microorganisms located in the periodontal tissues play an important role as potential initiators of immune-mediated inflammatory conditions at distant sites[2]. Studies have shown that the microbiota associated with PD is different from that in health, and the chronic inflammatory response induced by salivary microbiota plays an important role in the development of PD.

Objectives: Study to evaluate and quantify the differences in the composition of salivary microbiota in patients with PD, and investigate the correlation between salivary microbiota in patients with PD and clinical variables.

Methods: In the same race, 34 salivary samples of patients with PD and 28 salivary samples of periodontal health controls (HC) were collected for 16S rRNA gene sequencing. Compare salivary microbiota alpha-diversity, beta-diversity and microbial composition (at the phylum and genus levels) were used to determine differences in salivary microbiota characteristics between periodontitis patients and periodontal health controls. LetSe analysis was carried out to identify differentially abundant genera. The correlation between different taxa and clinical variables was calculated by the Spearman rank test.

Results: Consistent with the observed diversity trend, compared with periodontal health, the richness of patients with periodontitis is relatively high (P<0.05, Figure 1a), which indicates that the diversity of salivary microbiome in patients with periodontitis is significantly higher. The Beta diversity based on Bray Curtis distance at the species level demonstrated a significant difference in microbial communities between periodontitis patients and periodontal health (analysis of variance, r2=0.094, p=0.001, Figure 1b). At different phylogenetic levels, the 10 selected taxonomic biomarkers showed strong discrimination ability, with log10 LDA score >4.0 (Figure 1c-d). Specifically, at the phylum level, the Firmicutes/phylum frequency of periodontitis patients is lower, while the Spirochaetota frequency is higher. Patients with periodontitis have more genus Treponema at the genus level (Figure 1c-d). PICRUSt analysis found that in the KEGG pathway, the function of microbial genes related to amino acid metabolism in the salivary microbiota of periodontitis patients was higher (Figure 1h). Treponema was positively correlated with periodontal probing depth (PPD), Total, plaque index (PI) and periodontitis extent Ca. Sipirochaetota was positively correlated with PPD Total, PI (p<0.05, Figure 1i).

Conclusion: Specific salivary microbiota played an important role in the pathogenesis of periodontitis, which may help to diagnose or determine individual susceptibility to periodontitis by detecting salivary microbiota.

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